

SEQUENCE LISTING

<110> GROGER, HARALD
 WERNER, HELGE
 ALTENBUCHNER, JOSEF
 MENZEL, ANNE
 HUMMEL, WERNER

<120> PROCESS FOR PREPARING OPTICALLY ACTIVE AMINO ACIDS USING A
 WHOLE-CELL CATALYST

<130> 294227US-10757-9350-0-X PCT

<140> 10/593,567

<141> 2006-09-20

<150> PCT/EP2005/002933

<151> 2005-03-18

<150> DE 102004014280.7

<151> 2004-03-22

<160> 13

<170> PatentIn version 3.5

<210> 1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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<223> Description of Artificial Sequence: Synthetic
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<223> Description of Artificial Sequence: Synthetic primer

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Leu Asn Gly Arg Tyr Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp	
110 115 120	
gat atg gat att atc cat gaa gaa act gac ttt gta aca ggt atc tca	436
Asp Met Asp Ile Ile His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser	
125 130 135	
cca tca ttc ggt tct tct ggt aac cca tct ccg gta act gca tac ggt	484
Pro Ser Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly	
140 145 150 155	
gtt tac cgt ggt atg aaa gca gct gca aaa gaa gct ttc ggt act gac	532
Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp	
160 165 170	
aat tta gaa gga aaa gta att gct gtt caa ggc gtt ggt aac gta gca	580
Asn Leu Glu Gly Lys Val Ile Ala Val Gln Gly Val Gly Asn Val Ala	
175 180 185	
tat cac cta tgc aaa cat tta cac gct gaa gga gca aaa tta att gtt	628
Tyr His Leu Cys Lys His Leu His Ala Glu Gly Ala Lys Leu Ile Val	
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aca gat att aat aaa gaa gct gta caa cgt gct gta gaa gaa ttc ggt	676
Thr Asp Ile Asn Lys Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly	
205 210 215	
gca tca gca gtt gaa cca aat gaa att tac ggt gtt gaa tgc gat att	724
Ala Ser Ala Val Glu Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile	
220 225 230 235	
tac gca cca tgt gca cta ggc gca aca gtt aat gat gaa act att cca	772
Tyr Ala Pro Cys Ala Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro	
240 245 250	
caa ctt aaa gca aaa gta atc gca ggt tct gcg aat aac caa tta aaa	820
Gln Leu Lys Ala Lys Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys	
255 260 265	
gaa gat cgt cat ggt gac atc att cat gaa atg ggt att gta tac gca	868
Glu Asp Arg His Gly Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala	
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Pro Asp Tyr Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu	
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tta tat gga tac aat aga gaa cgt gca cta aaa cgt gtt gag tct att	964
Leu Tyr Gly Tyr Asn Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile	
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Tyr Asp Thr Ile Ala Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile	

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gca act tat gta gcg gca gat cgt cta gct gaa gag cgc att gca agc				1060
Ala Thr Tyr Val Ala Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser				
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Ser Arg Arg				
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Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp																		
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Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala																		
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Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly																		
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Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala																		
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Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr																		
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Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile																		
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His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser																		
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Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
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Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
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Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
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 <213> Candida boidinii

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tgg tta aaa gat caa ggt cat gaa cta att act act tct gat aaa gaa     144
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          35          40          45

ggt gaa aca agt gaa ttg gat aaa cat atc cca gat gct gat att atc     192
Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile
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atc acc act cct ttc cat cct gct tat atc act aag gaa aga ctt gac     240
Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
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aag gct aag aac tta aaa tta gtc gtt gtc gct ggt gtt ggt tct gat     288
Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
          85          90          95

cac att gat tta gat tat att aat caa aca ggt aag aaa atc tca gtc     336
His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
          100          105          110

ctg gaa gtt aca ggt tct aat gtt gtc tct gtt gct gaa cac gtt gtc     384
Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
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atg acc atg ctt gtc ttg gtt aga aat ttc gtt cca gca cat gaa caa     432
Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
          130          135          140

att att aac cac gat tgg gag gtt gct gct atc gct aag gat gct tac     480
Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
          145          150          155          160

gat atc gaa ggt aaa act atc gct acc att ggt gct ggt aga att ggt     528
Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
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tac aga gtc ttg gaa aga tta ctc cca ttt aat cca aaa gaa tta tta     576
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Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile	
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Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn	
225 230 235 240	
aag gaa tta tta tct aaa ttt aaa aaa ggt gct tgg tta gtc aat acc	768
Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr	
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gca aga ggt gct att gct gtt gct gaa gat gtt gca gca gct tta gaa	816
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260 265 270	
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Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro	
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Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln	
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Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu	
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tac gtt act aaa gct tac ggt aaa cac gat aag aaa taa	1095
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<210> 8

<211> 364

<212> PRT

<213> Candida boidinii

<400> 8

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Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
    65              70              75              80

Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
          85              90              95

His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
    100              105              110

Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
    115              120              125

Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
    130              135              140

Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
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Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
          165              170              175

Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu
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Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly
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Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile
    210              215              220

Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
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Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr
          245              250              255

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Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu
260 265 270

Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
275 280 285

Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
290 295 300

Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln
305 310 315 320

Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr
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<211> 5686

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Plasmid pAM3.25

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5686

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Plasmid pAM10.1

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Met Glu Pro Lys Thr Lys Lys Gln Arg Ser Leu Tyr Ile Pro Tyr Ala
10             15             20             25

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Gly Pro Val Leu Leu Glu Phe Pro Leu Leu Asn Lys Gly Ser Ala Phe
30             35             40

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Ser Met Glu Glu Arg Arg Asn Phe Asn Leu Leu Gly Leu Leu Pro Glu
45             50             55

gtg gtc gaa acc atc gaa gaa caa gcg gaa cga gca tgg atc cag tat 243
Val Val Glu Thr Ile Glu Glu Gln Ala Glu Arg Ala Trp Ile Gln Tyr
60             65             70

cag gga ttc aaa acc gaa atc gac aaa cac atc tac ctg cgt aac atc 291
Gln Gly Phe Lys Thr Glu Ile Asp Lys His Ile Tyr Leu Arg Asn Ile
75             80             85

cag gac act aac gaa acc ctc ttc tac cgt ctg gta aac aat cat ctt 339
Gln Asp Thr Asn Glu Thr Leu Phe Tyr Arg Leu Val Asn Asn His Leu
90             95             100             105

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Glu Arg Phe Ser Glu Ile Tyr Arg Arg Ser Arg Gly Val Phe Ile Ser	
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Tyr Gln Asn Arg His Asn Met Asp Asp Ile Leu Gln Asn Val Pro Asn	
140 145 150	
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His Asn Ile Lys Val Ile Val Val Thr Asp Gly Glu Arg Ile Leu Gly	
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Ser Leu Tyr Thr Ala Cys Gly Gly Ile Ser Pro Ala Tyr Thr Leu Pro	
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Arg Arg Thr Ser Ile
570

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<220>
<223> Description of Unknown: Plasmid sequence

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Pro Leu Leu Asn Lys Gly Ser Ala Phe Ser Met Glu Glu Arg Arg Asn
          35          40          45

Phe Asn Leu Leu Gly Leu Leu Pro Glu Val Val Glu Thr Ile Glu Glu
          50          55          60

Gln Ala Glu Arg Ala Trp Ile Gln Tyr Gln Gly Phe Lys Thr Glu Ile
          65          70          75          80

Asp Lys His Ile Tyr Leu Arg Asn Ile Gln Asp Thr Asn Glu Thr Leu
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Phe Tyr Arg Leu Val Asn Asn His Leu Asp Glu Met Met Pro Val Ile
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Gly Ile Ser Pro Ala Tyr Thr Leu Pro Val Val Leu Asp Val Gly Thr
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Pro Arg Ile Thr Asp Asp Glu Tyr Tyr Glu Phe Val Asp Glu Phe Ile
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Glu Met Ile Ile Ser Gln Thr Gln Arg Glu Gly Leu Ser Glu Glu Ala
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Val Ala Thr Gly Ser Pro Phe Asn Pro Val Val Trp Lys Asp Lys Ile
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Met Ser Ala Ser Glu Thr Leu Ala Gln Tyr Ser Pro Leu Val Leu Asn
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